AMENDMENTS TO THE SPECIFICATION

Please replace Fig. 3 with the substitute Fig. 3 (two pages) provided.

Please replace page 8 of the Specification with the following replacement page:

polynucleotide when each base in the first polynucleotide is paired with its complementary base. Complementary bases are, generally, A and T (or A and U), or C and G. "Complement" is used herein as a synonym from "complementary polynucleotide", "complementary nucleic acid" and "complementary nucleotide sequence".

As used in this disclosure, the term "percent homology" of two amino acid sequences or of two nucleic acid sequences is determined using the algorithm of Karlin and Altschul (Karlin and Altschul, 1990. Proc. Natl. Acad. Sci. USA 87:22264-2268) modified as in Karlin and Altschul (Karlin and Altschul, 1993. Proc. Natl. Acad. Sci. USA 90:5873-5877).Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (Altschul, et al., 1990. J. Mol. Biol. 215:403-410). Blast nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. Blast protein searches are performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a referenced polypeptide. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Altschul, et al. Nucleic Acids Res. 25:3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (XBLAST and NBLAST) are used. See http://www.ncbi.nlm.nih.gov.

The term "functional derivatives" includes "fragments," "degenerate variants," "mutants," "variants," and "chemical derivatives." When referring to a polypeptide, the term "fragment" is meant to refer to any polypeptide subset of GBS phage lysin having the amino acid sequence shown in SEQ ID NO:2. In one embodiment, the fragment is at least 5 amino acids in length; however, the fragments may be of greater length in alternate embodiments. In one embodiment, the polypeptide fragment may contain the AXE domain (amino acids 6-107), the Acm domain (amino acids 145-344), or both. Such polypeptide fragments may be used as immunogens to generate antibodies reactive against the full length GBS phage lysin protein. Fragments of the disclosure may be assayed for GBS phage lysin activity using the methods described herein. When referring to a polynucleotide, the term "fragment" is

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